

Search History

SCORE Search Results Details for Application 09522753 and Search Result us-09-522-753c-4.rge.

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2006, 05:48:17 ; Search time 30835 Seconds
(without alignments)
17754.301 Million cell updates/sec

Title: US-09-522-753C-4
Perfect score: 8561
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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
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2	8469.4	98.9	8854	2	CS186449 Sequence
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4	8238.8	96.2	9053	2	AR447713 Sequence
5	8058.6	94.1	8548	5	AY965853 Homo sapi
6	5475	64.0	5989	5	HSU37146 Human silen ←
7	5048.4	59.0	8544	6	AF125671 Mus muscu
8	4992.8	58.3	8388	6	AF113001 Mus muscu
9	4389.4	51.3	7465	6	AF113002 Mus muscu
10	4253.8	49.7	4686	5	AB209089 Homo sapi
11	3963.8	46.3	6339	2	CQ722208 Sequence
12	2773.8	32.4	2842	5	BC004326 Homo sapi
13	2628	30.7	2930	5	S83390 T3 receptor
14	1715	20.0	2964	6	BC047524 Mus muscu
c 15	1146.2	13.4	205283	5	AC073916 Homo sapi
16	956.8	11.2	161970	12	AC027706 Homo sapi
17	898.4	10.5	956	2	BD270289 Human nuc
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20	898.4	10.5	956	2	AX342140 Sequence
21	898.4	10.5	956	2	AX441143 Sequence
22	856.4	10.0	1925	11	CR926317 Xenopus t
23	854.6	10.0	1896	11	BC082706 Xenopus l
24	854.6	10.0	1917	11	BC054296 Xenopus l
c 25	744.2	8.7	79494	12	AC068837 Homo sapi
26	652.8	7.6	752	2	CQ769363 Sequence
27	650	7.6	650	2	AX677743 Sequence
28	631.6	7.4	7949	5	AB028970 Homo sapi
29	630	7.4	7940	2	CQ847916 Sequence
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35	626.8	7.3	3120	5	AF303586 Homo sapi
36	626.8	7.3	8018	5	AF087856 Homo sapi
37	615.8	7.2	7264	6	BC086657 Mus muscu
38	572.2	6.7	8626	11	BC099620 Xenopus t
39	570	6.7	725	7	BV448749 NCOR2_795
40	568.4	6.6	8959	11	AF495886 Xenopus l
41	555	6.5	555	2	AX677866 Sequence
c 42	554.8	6.5	560	5	HSU80761 Homo sapien
43	553.6	6.5	560	5	HSU80750 Homo sapien
c 44	542.4	6.3	718	2	AX753058 Sequence
45	540.6	6.3	1891	5	BC050594 Homo sapi
46	534	6.2	534	2	AX778323 Sequence
47	533.4	6.2	1850	5	BC058511 Homo sapi
48	533.2	6.2	1808	5	BC068996 Homo sapi
49	531.8	6.2	1741	5	BC056862 Homo sapi
50	516	6.0	1152	11	AY498876 Xenopus l
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	56	472.4	5.5	219339	12	AC121005	AC121005 Rattus no
c	57	472.4	5.5	254449	12	AC097560	AC097560 Rattus no
	58	458.8	5.4	527	2	CQ923115	CQ923115 Sequence
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ALIGNMENTS

RESULT 1

AF113003

LOCUS AF113003 8561 bp mRNA linear PRI 20-MAR-1999

DEFINITION Homo sapiens silencing mediator of retinoic acid and thyroid hormone receptor alpha mRNA, complete cds.

ACCESSION AF113003

VERSION AF113003.1 GI:4454551

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8561)

AUTHORS Ordentlich,P., Downes,M., Xie,W., Genin,A., Spinner,N.B. and Evans,R.M.

TITLE Unique forms of human and mouse nuclear receptor corepressor SMRT

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2639-2644 (1999)

PUBMED 10077563

REFERENCE 2 (bases 1 to 8561)

AUTHORS Downes,M.R., Ordentlich,P. and Evans,R.M.

TITLE Direct Submission

JOURNAL Submitted (11-DEC-1998) Gene Expression Laboratory, The Salk Institute for Biological Studies, 10010 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

source

Location/Qualifiers

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/chromosome="12"

/map="12q24"

/tissue_type="pituitary"

CDS

2. .7555

/function="transcriptional co-repressor"

/note="hSMRT alpha; longer isoform than previously reported"

/codon_start=1

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/protein_id="AAD20946.1"

/db_xref="GI:4454552"

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IESKHSRLVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAM
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OM nucleic - nucleic search, using sw model

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Run on:      July 30, 2006, 05:57:58 ; Search time 1397 Seconds
              (without alignments)
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Title:          US-09-522-753C-4
Perfect score:  8561
Sequence:       1 catgtcgggctccacacagc.....caaaaaaaaaaaaaaaaaaaaaa 8561
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Minimum DB seq length: 0.
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 60 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	8238.8	96.2	9053	3	US-09-976-594-306	Sequence 306, App
2	630	7.4	7912	3	US-09-949-016-3804	Sequence 3804, Ap
3	630	7.4	7940	3	US-09-632-033B-1	Sequence 1, Appli
4	629.6	7.4	7780	3	US-09-632-033B-2	Sequence 2, Appli
5	311.2	3.6	312	3	US-09-513-999C-33415	Sequence 33415, A
6	187.8	2.2	789	4	US-09-297-648-4382	Sequence 4382, Ap
7	142	1.7	1922	2	US-08-372-652-9	Sequence 9, Appli
8	142	1.7	1922	7	PCT-US95-16311-9	Sequence 9, Appli
c 9	133.4	1.6	350	4	US-09-880-107-341	Sequence 341, App
10	107.8	1.3	3489	2	US-08-728-323A-1	Sequence 1, Appli
11	107.8	1.3	3489	3	US-09-298-568-1	Sequence 1, Appli
12	107.8	1.3	3489	3	US-09-410-399-1	Sequence 1, Appli
13	107.8	1.3	3489	3	US-09-894-273-1	Sequence 1, Appli
c 14	107.8	1.3	32207	2	US-08-770-379-20	Sequence 20, Appl
c 15	107.8	1.3	32207	3	US-08-757-669A-20	Sequence 20, Appl
c 16	107.8	1.3	32207	3	US-09-230-371A-20	Sequence 20, Appl
17	104.6	1.2	187595	3	US-09-949-016-15546	Sequence 15546, A
18	98.8	1.2	1337	4	US-09-297-648-4735	Sequence 4735, Ap
19	96.2	1.1	1926	3	US-09-249-585A-2	Sequence 2, Appli
20	96.2	1.1	1926	3	US-09-410-399-3	Sequence 3, Appli
21	96.2	1.1	2580	3	US-09-050-863-2	Sequence 2, Appli
22	96.2	1.1	2580	3	US-09-359-081-2	Sequence 2, Appli
c 23	96.2	1.1	5452	2	US-09-130-114-1	Sequence 1, Appli
c 24	96.2	1.1	8705	3	US-09-647-344A-14	Sequence 14, Appl
25	96.2	1.1	9600	3	US-08-910-647-1	Sequence 1, Appli
26	96.2	1.1	9600	3	US-09-620-925-1	Sequence 1, Appli
27	96.2	1.1	10596	2	US-07-884-811-15	Sequence 15, Appl
28	96.2	1.1	10596	2	US-07-885-971-15	Sequence 15, Appl
29	96.2	1.1	10596	2	US-08-087-783A-15	Sequence 15, Appl
30	96.2	1.1	10596	2	US-08-194-088B-15	Sequence 15, Appl
31	96.2	1.1	10596	2	US-08-194-087-15	Sequence 15, Appl
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c 33	96.2	1.1	16080	3	US-09-724-566A-48	Sequence 48, Appl
c 34	96.2	1.1	16080	3	US-09-471-669A-48	Sequence 48, Appl
35	94.8	1.1	127	3	US-09-680-420A-17	Sequence 17, Appl
36	94.8	1.1	127	4	US-09-833-031A-17	Sequence 17, Appl
c 37	94.8	1.1	601	3	US-09-949-016-135614	Sequence 135614,
38	93	1.1	94	3	US-09-513-999C-29269	Sequence 29269, A
39	92	1.1	1852	3	US-09-969-852-4	Sequence 4, Appli
c 40	90	1.1	1926	3	US-09-249-585A-4	Sequence 4, Appli
c 41	90	1.1	1931	2	US-09-130-114-2	Sequence 2, Appli
c 42	89.8	1.0	7218	2	US-08-232-463-14	Sequence 14, Appl
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44	86.2	1.0	1995	2	US-08-317-844B-3	Sequence 3, Appli
c 45	85.4	1.0	16442	3	US-08-781-891-208	Sequence 208, App
c 46	85.4	1.0	16442	3	US-09-618-166-208	Sequence 208, App
47	82.8	1.0	767677	3	US-09-949-016-12147	Sequence 12147, A
48	82.8	1.0	767677	3	US-09-949-016-17361	Sequence 17361, A
49	82.4	1.0	2093	3	US-10-104-047-1666	Sequence 1666, Ap
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53	81.4	1.0	9551	2	US-08-056-200-93	Sequence 93, Appl
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c 55	80.2	0.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 56	79.4	0.9	150394	3	US-09-949-016-13042	Sequence 13042, A
57	79.2	0.9	1588	3	US-09-490-291-7	Sequence 7, Appli

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ALIGNMENTS

RESULT 1

US-09-976-594-306

; Sequence 306, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROID

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594.

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 306

; LENGTH: 9053

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 898877.6

; NAME/KEY: unsure

; LOCATION: 2006, 2012

; OTHER INFORMATION: a, t, c, g, or other

US-09-976-594-306

Query Match 96.2%; Score 8238.8; DB 3; Length 9053;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 8456; Conservative 0; Mismatches 38; Indels 95; Gaps 10;

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Qy      181 GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCGGGAATGAACGGTCCCA 240
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Db      699 GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCGGGAATGAACGGTCCCA 758

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Qy      301 GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCTGCTGCGACC 360
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2006, 09:26:05 ; Search time 8988 Seconds
(without alignments)
11703.877 Million cell updates/sec

Title: US-09-522-753C-4
Perfect score: 8561
Sequence: 1 catgtcgggctccacacagc.....caaaaaaaaaaaaaaaaaaaaaa 8561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : Published_Applications_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	8561	100.0	8561	13	US-11-052-344-1	Sequence 1, Appli
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9	7334.6	85.7	7521	3	US-09-819-104A-3	Sequence 3, Appli
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14	2628	30.7	2930	6	US-10-146-473-14	Sequence 14, Appl
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19	898.4	10.5	956	3	US-09-887-527-42	Sequence 42, Appl
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22	630	7.4	7940	9	US-10-473-974-191	Sequence 191, App
23	630	7.4	7940	10	US-10-887-553A-664	Sequence 664, App
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25	630	7.4	7940	10	US-10-745-237-221	Sequence 221, App
26	630	7.4	7940	16	US-11-245-147-191	Sequence 191, App
27	626.8	7.3	2745	7	US-10-414-692-15	Sequence 15, Appl
c 28	553.6	6.5	692	6	US-10-027-632-102554	Sequence 102554,
c 29	553.6	6.5	692	6	US-10-027-632-102555	Sequence 102555,
c 30	553.6	6.5	692	7	US-10-027-632-102554	Sequence 102554,
c 31	553.6	6.5	692	7	US-10-027-632-102555	Sequence 102555,
c 32	542.4	6.3	718	9	US-10-278-698-515	Sequence 515, App
c 33	542.4	6.3	718	9	US-10-278-698-1031	Sequence 1031, Ap
34	444.4	5.2	91141	6	US-10-087-192-649	Sequence 649, App
35	409.4	4.8	427	10	US-10-779-543-12895	Sequence 12895, A
36	376	4.4	872	10	US-10-779-543-8757	Sequence 8757, Ap
37	370	4.3	381	3	US-09-918-995-7653	Sequence 7653, Ap
38	314.4	3.7	458	3	US-09-918-995-20064	Sequence 20064, A
39	268.6	3.1	520	3	US-09-920-300A-485	Sequence 485, App
40	268.6	3.1	520	6	US-10-033-528-485	Sequence 485, App
41	268.6	3.1	520	7	US-10-099-926-485	Sequence 485, App
42	268.6	3.1	520	10	US-10-961-527-485	Sequence 485, App
43	258.4	3.0	3969	7	US-10-006-285-471	Sequence 471, App
44	211.4	2.5	499	3	US-09-918-995-19696	Sequence 19696, A
c 45	191.4	2.2	390	7	US-10-355-716-86	Sequence 86, Appl
c 46	190.6	2.2	559	16	US-11-136-527-1693	Sequence 1693, Ap
47	190.6	2.2	559	16	US-11-136-527-5789	Sequence 5789, Ap
48	187.8	2.2	789	10	US-10-779-543-5226	Sequence 5226, Ap
c 49	186.2	2.2	609	4	US-09-925-065A-841377	Sequence 841377,
c 50	186.2	2.2	609	5	US-09-925-065A-841377	Sequence 841377,
51	186.2	2.2	658	6	US-10-027-632-102075	Sequence 102075,
52	186.2	2.2	658	6	US-10-027-632-102076	Sequence 102076,
53	186.2	2.2	658	7	US-10-027-632-102075	Sequence 102075,
54	186.2	2.2	658	7	US-10-027-632-102076	Sequence 102076,

c	55	180	2.1	733	6	US-10-027-632-151931	Sequence 151931,
c	56	180	2.1	733	7	US-10-027-632-151931	Sequence 151931,
	57	171	2.0	504	7	US-10-355-716-87	Sequence 87, Appl
c	58	161	1.9	888	12	US-10-301-480-553156	Sequence 553156,
c	59	161	1.9	888	12	US-10-301-480-1166565	Sequence 1166565,
c	60	159.6	1.9	198	3	US-09-960-352-7433	Sequence 7433, Ap

ALIGNMENTS

RESULT 1

US-10-174-014-11

; Sequence 11, Application US/10174014

; Publication No. US20040005292A1

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION

; FILE REFERENCE: PTS-0012

; CURRENT APPLICATION NUMBER: US/10/174,014

; CURRENT FILING DATE: 2002-06-17

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 11

; LENGTH: 8561

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)...(7555)

US-10-174-014-11

Query Match 100.0%; Score 8561; DB 7; Length 8561;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 8561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CATGTCGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC	60
Db	1	CATGTCGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC	60
Qy	61	GCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGACGCACACGGACGTCGGGCTCCT	120
Db	61	GCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGACGCACACGGACGTCGGGCTCCT	120
Qy	121	GGAGTACCAGCACCCTCCCGCGACTATGCCTCCACCTGTCGCCGGGCTCCATCATCCA	180
Db	121	GGAGTACCAGCACCCTCCCGCGACTATGCCTCCACCTGTCGCCGGGCTCCATCATCCA	180
Qy	181	GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCCGGAATGAACGGTCCCA	240
Db	181	GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCCGGAATGAACGGTCCCA	240
Qy	241	GGAGCTCCACCTGCGGCCAGAGTCCCACTCATACCTGCCCGAGCTGGGGAAGTCAGAGAT	300
Db	241	GGAGCTCCACCTGCGGCCAGAGTCCCACTCATACCTGCCCGAGCTGGGGAAGTCAGAGAT	300
Qy	301	GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCTGCTGCGACC	360
Db	301	GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCTGCTGCGACC	360

SCORE Search Results Details for Application 09522753 and Search Result us-09-522-753c- 4.rst.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
-------------------------------------	---	---	-------------------------------	--

This page gives you Search Results detail for the Application 09522753 and Search Result us-09-522-753c-4.rst.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2006, 05:48:19 ; Search time 23790 Seconds
(without alignments)
20122.968 Million cell updates/sec

Title: US-09-522-753C-4
Perfect score: 8561
Sequence: 1 catgtcgggtccacacagc.....caaaaaaaaaaaaaaaaaaaaaa 8561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5314.4	62.1	8660	6	AK147394	AK147394 Mus muscu
2	5140.2	60.0	7372	14	AY412686	AY412686 Homo sapi
3	4216.6	49.3	6836	14	AY412687	AY412687 Pan trogl
4	3522.8	41.1	5672	6	AK147308	AK147308 Mus muscu
5	3315.2	38.7	7013	14	AY412688	AY412688 Mus muscu
6	1577.4	18.4	3596	6	AK170097	AK170097 Mus muscu
7	1473.6	17.2	2000	6	BC033087	BC033087 Homo sapi
8	1297.4	15.2	1362	6	BC020427	BC020427 Homo sapi
9	887.8	10.4	1093	3	BM909096	BM909096 AGENCOURT
10	868.6	10.1	965	3	BM555371	BM555371 AGENCOURT
11	841.8	9.8	846	3	BU557144	BU557144 AGENCOURT
12	815.6	9.5	1126	2	BM553310	BM553310 AGENCOURT
13	798.2	9.3	984	3	BQ690869	BQ690869 AGENCOURT
14	796.4	9.3	1051	2	BM423558	BM423558 AGENCOURT
15	796.2	9.3	1159	3	BM802749	BM802749 AGENCOURT
16	795.2	9.3	1057	2	BM477568	BM477568 AGENCOURT
17	787.6	9.2	1022	3	BM910785	BM910785 AGENCOURT
18	779	9.1	1010	3	BM915686	BM915686 AGENCOURT
19	776.6	9.1	875	3	BQ711119	BQ711119 AGENCOURT
20	774.6	9.0	892	3	BU538827	BU538827 AGENCOURT
21	768.8	9.0	1036	3	BM910476	BM910476 AGENCOURT
22	766.2	8.9	1030	3	BM558844	BM558844 AGENCOURT
23	760.8	8.9	882	4	BX397973	BX397973 BX397973
24	747.6	8.7	868	4	BX368971	BX368971 BX368971
25	746.8	8.7	882	3	BU180236	BU180236 AGENCOURT
26	746	8.7	923	4	BX390462	BX390462 BX390462
27	744.2	8.7	1075	2	BM461469	BM461469 AGENCOURT
c 28	740	8.6	916	3	BQ892847	BQ892847 AGENCOURT
29	737.4	8.6	1045	3	BM560255	BM560255 AGENCOURT
30	730.8	8.5	1038	3	BM910704	BM910704 AGENCOURT
31	730.6	8.5	1066	2	BM471347	BM471347 AGENCOURT
32	728.4	8.5	882	2	BI089430	BI089430 602854662
33	720.8	8.4	769	4	BX368972	BX368972 BX368972
34	712.6	8.3	898	3	BU172348	BU172348 AGENCOURT
35	711.8	8.3	958	2	BG831424	BG831424 602766347
c 36	711.4	8.3	880	8	CV806970	CV806970 AGENCOURT
37	711	8.3	875	3	BQ691710	BQ691710 AGENCOURT
38	707.4	8.3	923	3	BU184403	BU184403 AGENCOURT
39	706.8	8.3	1094	3	BM560912	BM560912 AGENCOURT
40	703	8.2	876	2	BG252161	BG252161 602365028
41	703	8.2	1067	2	BM472005	BM472005 AGENCOURT
42	700.6	8.2	928	3	BU164114	BU164114 AGENCOURT
c 43	695.8	8.1	772	5	CF135847	CF135847 UI-HF-BNO
c 44	692.8	8.1	727	3	BU632778	BU632778 UI-H-FE1-
45	692	8.1	830	8	CO648233	CO648233 ILLUMIGEN
46	688	8.0	861	3	BU191146	BU191146 AGENCOURT
c 47	683	8.0	737	5	CD742837	CD742837 UI-H-FT2-
48	679.6	7.9	1087	2	BG252257	BG252257 602365136
c 49	678.8	7.9	784	4	CB321637	CB321637 UI-CF-EN1
50	674.2	7.9	787	7	BE793487	BE793487 601588814
51	672	7.8	1113	3	BM811122	BM811122 AGENCOURT
52	670.8	7.8	674	9	CX873148	CX873148 HESC4_77
53	668.4	7.8	804	7	BE728145	BE728145 601563413

54	668.4	7.8	1032	3	BQ070408	BQ070408	AGENCOURT
55	664.4	7.8	900	3	BQ214358	BQ214358	AGENCOURT
c 56	663.4	7.7	764	3	BM981385	BM981385	UI-CF-EN1
57	661	7.7	700	7	BE900740	BE900740	601673910
58	660.6	7.7	1111	7	BF307042	BF307042	601889875
59	652	7.6	743	8	CO401621	CO401621	AGENCOURT
60	651	7.6	887	3	BU542258	BU542258	AGENCOURT

ALIGNMENTS

RESULT 1

AK147394

LOCUS AK147394 8660 bp mRNA linear HTC 21-SEP-2005

DEFINITION Mus musculus cDNA, RIKEN full-length enriched library, clone:M5C1029F22 product:nuclear receptor co-repressor 2, full insert sequence.

ACCESSION AK147394

VERSION AK147394.1 GI:74184520

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,

SCORE Search Results Details for Application 09522753 and Search Result us-09-522-753c-4.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 21:46:53 ; Search time 793 Seconds
(without alignments)
17098.629 Million cell updates/sec

Title: US-09-522-753C-4
Perfect score: 8561
Sequence: 1 catgtcgggctccacacagc.....caaaaaaaaaaaaaaaaaaaaaa 8561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : Published Applications_NA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	8561	100.0	8561	8	US-11-283-329-203	Sequence 203, App
2	8344.6	97.5	8686	8	US-11-266-748A-23081	Sequence 23081, A
c 3	1311	15.3	1324	8	US-11-266-748A-225635	Sequence 225635,
4	1311	15.3	1324	8	US-11-266-748A-240202	Sequence 240202,
c 5	1283.6	15.0	1483	8	US-11-266-748A-247117	Sequence 247117,
c 6	1220	14.3	1220	8	US-11-266-748A-82872	Sequence 82872, A
c 7	1220	14.3	1220	8	US-11-266-748A-111459	Sequence 111459,
8	1220	14.3	1220	8	US-11-266-748A-135683	Sequence 135683,
9	1069.4	12.5	1656	8	US-11-266-748A-90734	Sequence 90734, A
c 10	1069.4	12.5	1656	8	US-11-266-748A-143545	Sequence 143545,
c 11	1008.4	11.8	1260	8	US-11-266-748A-368438	Sequence 368438,
12	1008.4	11.8	1260	8	US-11-266-748A-451817	Sequence 451817,
13	981.6	11.5	1000	8	US-11-266-748A-116592	Sequence 116592,
c 14	981.6	11.5	1000	8	US-11-266-748A-158756	Sequence 158756,
15	981.6	11.5	1000	8	US-11-266-748A-287269	Sequence 287269,
c 16	981.6	11.5	1000	8	US-11-266-748A-338698	Sequence 338698,
17	981.6	11.5	1000	8	US-11-266-748A-397920	Sequence 397920,
c 18	981.6	11.5	1000	8	US-11-266-748A-468966	Sequence 468966,
c 19	907.8	10.6	1148	8	US-11-266-748A-183721	Sequence 183721,
c 20	907.8	10.6	1148	8	US-11-266-748A-191121	Sequence 191121,
21	907.8	10.6	1148	8	US-11-266-748A-240203	Sequence 240203,
22	751.6	8.8	954	8	US-11-266-748A-170725	Sequence 170725,
c 23	666.8	7.8	1090	8	US-11-266-748A-370741	Sequence 370741,
24	666.8	7.8	1090	8	US-11-266-748A-454120	Sequence 454120,
25	630	7.4	7940	8	US-11-266-748A-29708	Sequence 29708, A
26	630	7.4	7940	8	US-11-283-329-195	Sequence 195, App
27	626.8	7.3	3120	8	US-11-283-329-197	Sequence 197, App
28	626.8	7.3	8018	8	US-11-266-748A-22953	Sequence 22953, A
29	613.8	7.2	629	8	US-11-266-748A-54126	Sequence 54126, A
30	552	6.4	1089	8	US-11-266-748A-98563	Sequence 98563, A
c 31	552	6.4	1089	8	US-11-266-748A-151374	Sequence 151374,
c 32	543.2	6.3	600	8	US-11-266-748A-177072	Sequence 177072,
33	543.2	6.3	600	8	US-11-266-748A-247938	Sequence 247938,
34	540.6	6.3	1891	8	US-11-266-748A-27715	Sequence 27715, A
35	495.6	5.8	513	8	US-11-266-748A-8487	Sequence 8487, Ap
c 36	484.6	5.7	514	8	US-11-266-748A-179122	Sequence 179122,
37	484.6	5.7	514	8	US-11-266-748A-248437	Sequence 248437,
38	465	5.4	530	8	US-11-266-748A-103238	Sequence 103238,
c 39	465	5.4	530	8	US-11-266-748A-156049	Sequence 156049,
40	456.2	5.3	590	8	US-11-266-748A-170524	Sequence 170524,
41	442.6	5.2	911	8	US-11-266-748A-186813	Sequence 186813,
42	438	5.1	576	8	US-11-266-748A-10968	Sequence 10968, A
43	245.8	2.9	539	8	US-11-266-748A-260913	Sequence 260913,
c 44	245.8	2.9	539	8	US-11-266-748A-321430	Sequence 321430,
45	240.6	2.8	260	8	US-11-266-748A-173616	Sequence 173616,
46	236.4	2.8	1266	8	US-11-266-748A-99378	Sequence 99378, A
c 47	236.4	2.8	1266	8	US-11-266-748A-152189	Sequence 152189,
48	219	2.6	629	8	US-11-266-748A-172360	Sequence 172360,
49	197	2.3	1165	8	US-11-266-748A-15619	Sequence 15619, A
50	197	2.3	1165	8	US-11-266-748A-21269	Sequence 21269, A
51	147.4	1.7	1556	8	US-11-266-748A-187638	Sequence 187638,
c 52	141	1.6	630	8	US-11-266-748A-172361	Sequence 172361,
53	139.8	1.6	798	8	US-11-266-748A-82871	Sequence 82871, A
54	139.8	1.6	798	8	US-11-266-748A-111458	Sequence 111458,
c 55	139.8	1.6	798	8	US-11-266-748A-135682	Sequence 135682,
56	134.6	1.6	2471	8	US-11-283-329-201	Sequence 201, App
57	134.6	1.6	3997	8	US-11-266-748A-23524	Sequence 23524, A
58	134.6	1.6	3997	8	US-11-283-329-199	Sequence 199, App

c	59	115	1.3	30191	6	US-10-540-898-631	Sequence 631, App
c	60	113.4	1.3	72352	6	US-10-540-898-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-11-283-329-203

; Sequence 203, Application US/11283329

; Publication No. US20060134670A1

; GENERAL INFORMATION:

; APPLICANT: Piu, Fabrice

; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR

; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS

; FILE REFERENCE: ACADIA.043A

; CURRENT APPLICATION NUMBER: US/11/283,329

; CURRENT FILING DATE: 2005-11-18

; PRIOR APPLICATION NUMBER: 60/629,811

; PRIOR FILING DATE: 2004-11-19

; NUMBER OF SEQ ID NOS: 242

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 203

; LENGTH: 8561

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)...(7555)

; OTHER INFORMATION: NCOR-2

US-11-283-329-203

Query Match 100.0%; Score 8561; DB 8; Length 8561;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 8561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	GGAGTACCAGCACCCTCCCGCGACTATGCCTCCACCTGTCGCCGGGCTCCATCATCCA	180
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Qy	361	GTCACCCCTGCTGGCCACGGGCCAGCCTGCGGGATCTGAAGACCTACCAAGGACCGTAG	420

**SCORE Search Results Details for Application
09522753 and Search Result us-09-522-753c-
4.rng.**

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FAO

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This page gives you Search Results detail for the Application 09522753 and Search Result us-09-522-753c-4.rng.

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: July 29, 2006, 13:26:29 ; Search time 3157 Seconds
(without alignments)
18907.006 Million cell updates/sec

Title: US-09-522-753C-4
Perfect score: 8561
Sequence: 1 catgtcgggctccacacagc.....caaaaaaaaaaaaaaaaaaaaaa 8561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 60 summaries
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8:  geneseqn2003as:*
9:  geneseqn2003bs:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8561	100.0	8561	12	ADG86298	Adg86298 Human SMR
2	8561	100.0	8561	12	ADN04304	Adn04304 Antipsori
3	8561	100.0	8561	14	AEB92295	Aeb92295 Human SMR
4	8561	100.0	8561	14	AED18610	Aed18610 Fibrotic
5	8515.2	99.5	8564	3	AAC74783	Aac74783 Human ORF
6	8479.2	99.0	8667	11	ACN44283	Acn44283 Human mRN
7	8469.4	98.9	8854	14	AED61908	Aed61908 Human nuc
8	8437.2	98.6	8533	13	ADQ84524	Adq84524 Human tum
9	8437.2	98.6	8533	13	ACN39603	Acn39603 Tumour-as
10	8344.6	97.5	8686	8	ACA62249	Aca62249 cDNA enco
11	8344.6	97.5	8686	10	ADL13811	Adl13811 Osteoarth
12	8344.6	97.5	8686	12	ADG86290	Adg86290 Human SMR
13	8344.6	97.5	8686	12	ADQ18920	Adq18920 Human sof
c 14	8242.2	96.3	9079	12	ADQ23294	Adq23294 Human sof
15	8238.8	96.2	9053	12	ADL12577	Adl12577 Human ste
16	7554	88.2	7554	12	ADJ92815	Adj92815 Human co-
17	7337.6	85.7	7524	10	ADL13812	Adl13812 Osteoarth
18	7334.6	85.7	7521	8	ACA62250	Aca62250 Human nuc
19	5475	64.0	5989	6	ABK84305	Abk84305 Human cDN
20	5048.4	59.0	8544	8	ACA62451	Aca62451 cDNA enco
21	5048.4	59.0	8544	14	ADZ61802	Adz61802 Murine Nc
22	4797	56.0	7386	8	ACA62452	Aca62452 Mouse nuc
23	4554.6	53.2	7534	11	ACN44281	Acn44281 Mouse mRN
24	2628	30.7	2930	10	ADC35130	Adc35130 Human bre
25	2628	30.7	2930	12	ADG86301	Adg86301 Human SMR
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27	1146.2	13.4	220756	12	ADG86300	Adg86300 Human SMR
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47	534	6.2	534	10	ADF79924	Adf79924 Leukaemia
48	494.6	5.8	2914	13	ADR07585	Adr07585 Full leng
49	458.8	5.4	527	13	ADU13876	Adu13876 Solid tum
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52	376	4.4	872	3	AAA02670	Aaa02670 Human col

53	370	4.3	381	9	ACH20441	Ach20441 Human adu
54	349.8	4.1	554	13	ADQ56131	Adq56131 Novel can
55	314.4	3.7	458	9	ACH32852	Ach32852 Human end
56	311.2	3.6	312	3	AAC29340	Aac29340 Human sec
c 57	291.6	3.4	710	4	AAI97539	Aai97539 Human neu
58	282.8	3.3	673	8	ACA57523	Aca57523 Human adi
59	268.6	3.1	520	6	ABK44934	Abk44934 cDNA enco
60	258.4	3.0	3969	10	ADI22661	Adi22661 Human liv

ALIGNMENTS

RESULT 1

ADG86298

ID ADG86298 standard; cDNA; 8561 BP.

XX

AC ADG86298;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human SMRT encoding cDNA SEQ ID NO:12.

XX

KW SMRT; silencing mediator for retinoid and thyroid hormone action;

KW SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic;

KW antirheumatic; antisense therapy; inflammatory disorder;

KW rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia;

KW breast cancer; human; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 2..7555

FT /*tag= a

FT /product= "SMRT"

XX

PN WO2003106645-A2.

XX

PD 24-DEC-2003.

XX

PF 17-JUN-2003; 2003WO-US018923.

XX

PR 17-JUN-2002; 2002US-00174014.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Freier SM, Dobie KW;

XX

DR WPI; 2004-082184/08.

DR P-PSDB; ADG86299.

DR GENBANK; NM_006312.

XX

PT Novel antisense compound targeted to nucleic acid encoding SMRT

PT (silencing mediator for retinoid and thyroid hormone action), useful for

PT treating animal having disease associated with SMRT such as cancer,

PT rheumatoid arthritis.

XX

PS Example 15; SEQ ID NO 12; 260pp; English.

XX

CC The present invention describes a compound (I) 8-50 nucleobases in length

CC targeted to a nucleic acid molecule encoding SMRT (silencing mediator for

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display Show Send to

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [AB028970](#). Reports ...[gi:5689430] The record has been replaced by [29421187](#)

Features Sequence

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DEFINITION Homo sapiens mRNA for KIAA1047 protein, partial cds.
ACCESSION AB028970
VERSION AB028970.1 GI:5689430
KEYWORDS .
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kikuno,R., Nagase,T., Ishikawa,K., Hirose,M., Miyajima,N.,
Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro
JOURNAL DNA Res. 6 (3), 197-205 (1999)
PUBMED [10470851](#)
REFERENCE 2 (bases 1 to 5872)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
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4981 aactgcacaa agtgagggga acagggtgca ggagagggat ctctagtttt tgtggttta
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5281 ccataatgtc tttaaatcac tcttctgtaa atagatgacc tttttgcagt gtatatcccc
5341 ttgctgtagt atctggtgta cttatgttca aatcagcgca tcaactttgg ggtgatttt
5401 taaaaatctt tttgtctatc tatcttttta accctagcct tctaaacaac ctcatacagc
5461 ccagttacat aatgttggct gtcacgggca ttgtactttt atctgatatt gtttctctca
```

5521 aattcagctt tccagtgatg tttaaaatct tgtgaaaatg tttagatttt taacacagac
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5641 taaatttcca gtgcaggctt taattttttt ttttcattag tagcactgaa aaaatattac
5701 tgcattggga tggtctagtt cagttttataa agtttttaaag gcttatttga ggcataacct
5761 actgttacgc aactgggtaa ttttaacctg cccctaagta ttccttttct cctgcatttg
5821 atgcagccca acaaagcttt tgttttgaaa taaatttgac taccctgtcc at

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